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**Part 1:** **TITLE, AUTHORS, APPROVALS, etc**

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| **Code assigned:** | ***2023.012D*** |  |
| **Short title:** Rename 22 species in the family *Iridoviridae* |
|  |

**Author(s) and email address(es)**

|  |  |
| --- | --- |
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| Thomas Barclay Waltzek |

**List the ICTV Study Group(s) that have seen this proposal**

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| *Iridoviridae* |

**ICTV Study Group comments and response of proposer**

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| The authors are the *Iridoviridae* Study Group |

**ICTV Study Group votes on proposal**

|  |  |
| --- | --- |
| **Study Group** | **Number of members** |
| **Votes support** | **Votes against** | **No vote** |
| *Iridoviridae* | 12 | 0 | 2 |
|  |  |  |  |

**Authority to use the name of a living person**

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| --- | --- |
| **Is any taxon name used here derived from that of a living person (Y/N)** | N |

|  |  |  |
| --- | --- | --- |
| **Taxon name** | **Person from whom the name is derived** | **Permission attached (Y/N)** |
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**Submission dates**

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| --- | --- |
| Date first submitted to SC Chair | 16 June 2023 |
| Date of this revision (if different to above) | 24 June 2023 |

**ICTV-EC comments and response of the proposer**

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**Part 3:** **TAXONOMIC PROPOSAL**

**Name of accompanying Excel module**

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| --- |
| 2023.012D.N.v2.Iridoviridae\_22renam.xlsx |

**Abstract**

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| This proposal is to rename 22 species in the family *Iridoviridae* using a binomial format as mandated by the ICTV. |

**Text of proposal**

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| Historically, species in the family *Iridoviridae* have not been named using a single set of unifying rules. For example, *Santee-Cooper ranavirus* (subfamily *Alphairidovirinae,* genus *Ranavirus*) was named after the reservoir (Santee-Cooper Reservoir in SC, USA) from which moribund largemouth bass (*Micropterus salmoides*) were investigated leading to the isolation and characterization of the virus (i.e., largemouth bass virus). In contrast, *Infectious spleen and kidney necrosis virus* and *Scale drop disease virus* (subfamily *Alphairidovirinae,* genus *Megalocytivirus*) were named based on the pathology observed in the respective hosts. The names of other species, such as *Lymphocystivirus disease virus 1-4* (subfamily *Alphairidovirinae,* genus *Lymphocystivirus*), reflect the genus to which they belong, the recognized disease (lymphocystis disease), and a numeral to serve as a unique identifier. An example of a current species name is *Santee-Cooper ranavirus*, of which largemouth bass virus is a member.In the proposed binomial format, the first word would be the name of the genus to which the viral species belongs. The second word (the species epithet) consists of joining two elements. The first element is the name of the genus of the host that harbours the virus, written in lower case letters. For iridoviruses that infect hosts from multiple genera, the name of a prominent host genus will be incorporated with preference given to the genus in which the virus was initially characterized. A taxonomic change to the name of a host genus that occurs after the associated iridovirus was initially characterized will not alter the iridovirus species epithet. The second element is a numeral to serve as a unique identifier. For example, largemouth bass (genus *Micropterus*) is a prominent host for the virus (largemouth bass virus) of the species *Santee-Cooper ranavirus*. Thus, *Santee-Cooper ranavirus* would become *Ranavirus micropterus1.* We do not recommend the classification of iridoviruses identified in the absence of host information.The proposed binomial species nomenclature should be easily implemented. Species names will convey the information that we consider to be important, such as a prominent host (i.e., genus) of the virus and a number to differentiate it from other viruses infecting the same host genus but belonging to separate species. |

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